CLAIMS

1. DNA sequence, a 5' regulatory element allowing the expression of a heterologous gene in a plant cell from a monocotyledonous plant, characterized in that it comprises, in the direction of transcription, a first DNA sequence, which is a functional fragment of the sequence of the maize H3C4 promoter, and a second DNA sequence, which is a functional fragment of the sequence of the first intron of rice actin.

2. Sequence according to claim 1, characterized in that the sequence of the maize H3C4 promoter is the *AluI* fragment of the maize H3C4 promoter.

3. Sequence according to claim 1, characterized in that the functional fragment of the sequence of the maize H3C4 promoter comprises the DNA sequence described by the sequence identifier No. 1 (SEQ ID NO: 1) or a sequence homologous to the said sequence.

4. Sequence according to claim 3, characterized in that the functional fragment of the sequence of the maize H3C4 promoter consists of the DNA sequence described by the sequence identifier No. 1.

5. Sequence according to one of claims 1 to 4, characterized in that the functional fragment of the first intron of rice actin comprises the DNA sequence described by the sequence identifier No. 2 (SEQ ID

NO: 2) or a sequence homologous to the said sequence.

6. Sequence according to claim 5, characterized in that the functional fragment of the first intron of rice actin consists of the DNA sequence described by the sequence identifier No. 2.

7. Sequence according to one of claims 1 to 6, characterized in that it comprises a neutral DNA fragment between the first and second DNA sequences.

8. DNA sequence, a 5' regulatory element allowing the expression of a heterologous gene in a plant cell from a monocotyledonous plant, characterized in that it comprises the DNA sequence represented by the sequence identifier No. 3 (SEQ ID NO: 3) or a sequence homologous to the said sequence.

9. DNA sequence according to claim 8, characterized in that it consists of the DNA sequence represented by the sequence identifier No. 3.

10. Chimeric gene comprising a coding sequence as well as heterologous regulatory elements at the 5' and 3' positions capable of functioning in plant cells from monocotyledonous plants or in monocotyledonous plants, characterized in that the 5' regulatory elements comprise the DNA sequence according to one of claims 1 to 9.

11. Chimeric gene according to claim 10, characterized in that the coding sequence is chosen from a gene encoding a selectable marker, a gene conferring on the transformed monocotyledonous plant

new agronomic properties, and a gene for enhancing the agronomic quality of the transformed monocotyledonous plant.

12. Chimeric gene according to claim 11, characterized in that the gene conferring new agronomic properties on the transformed monocotyledonous plants is chosen from a gene conferring tolerance to certain herbicides, a gene conferring tolerance to certain insects and a gene conferring tolerance to certain diseases.

13. Chimeric gene according to claim 12, characterized in that the gene conferring tolerance to certain herbicides is chosen from the *Bar* gene conferring tolerance to bialaphos, a gene encoding an appropriate EPSPS conferring resistance to herbicides having EPSPS as target, the gene encoding glyphosate oxidoreductase and a gene encoding an HPPD conferring tolerance to herbicides having HPPD as target.

14. Chimeric gene according to claim 13, characterized in that the gene conferring tolerance to certain herbicides is chosen from a gene encoding an EPSPS and a gene encoding an HPPD.

15. Chimeric gene according to claim 14, characterized in that the gene encoding an EPSPS is chosen from the double-mutant EPSPS and CP4.

16. Chimeric gene according to either of claims 14 and 15, characterized in that the sequence encoding an EPSPS or an HPPD is preceded by a sequence

encoding a transit peptide.

17. Chimeric gene according to claim 16, characterized in that the transit peptide is the optimized transit peptide.

18. Chimeric gene characterized in that it comprises, in the direction of transcription, a 5' regulatory sequence defined according to one of claims 1 to 9, functionally linked to a sequence encoding a fusion protein transit peptide/protein of interest, functionally linked to a 3' regulatory sequence.

19. Chimeric gene according to claim 16, characterized in that the protein of interest is an enzyme conferring tolerance to certain herbicides according to one of claims 13 to 15.

20. Chimeric gene according to claim 18, characterized in that the sequence encoding a fusion protein transit peptide/protein of interest is chosen from the sequence encoding the fusion protein OTP/double-mutant EPSPS and the sequence encoding the fusion protein OTP/CP4.

21. DNA sequence encoding a fusion protein OTP/CP4.

22. Fusion protein OTP/CP4.

23. Chimeric gene characterized in that it comprises, in the direction of transcription, an appropriate 5' regulatory sequence for ensuring the expression of a coding sequence in plants, functionally linked to a sequence encoding a fusion protein OTP/CP4,

optionally linked to a 3' regulatory sequence.

24. Cloning or expression vector for the transformation of a plant cell or of a plant, characterized in that it comprises, in addition to the chimeric gene according to one of claims 10 to 20 or 23, at least one replication origin.

25. Vector according to claim 24, characterized in that it is a plasmid.

26. Method of transforming plant cells, characterized in that a chimeric gene according to one of claims 10 to 20 or 23 is integrated.

27. Plant cell, characterized in that it contains at least one chimeric gene according to one of claims 10 to 20 or 23.

28. Transformed plant, characterized in that it comprises cells according to claim 27.

29. Transformed plant according to claim 28, characterized in that it is regenerated from the cells according to claim 27.

30. Transformed plant according to claim 28, characterized in that it is derived from the culture and/or the crossing of a transformed plant according to either of claims 28 and 29.

31. Seed of a transformed plant according to one of claims 28 to 30.

32. Method of controlling weeds in an area of a field comprising seeds or plants transformed with a chimeric gene comprising a sequence encoding an

enzyme conferring tolerance to a particular herbicide, which method consists in applying to the said area of the field a dose of the said particular herbicide which is toxic to the said weeds, without, however, substantially affecting the seeds or plants transformed with the said chimeric gene, characterized in that the said chimeric gene is defined according to one of claims 13 to 20 or 23.

33. Method of culturing plants transformed with a chimeric gene comprising a sequence encoding an enzyme conferring tolerance to a particular herbicide defined according to one of claims 13 to 20 or 23, characterized in that the method consists in planting the seeds of the said transformed plants in an area of a field which is appropriate for the culture of the said plants, in applying to the said area of the said field a dose of the said particular herbicide which is toxic to weeds should weeds be present, without substantially affecting the said seeds or the said transformed plants, and then in harvesting the cultivated plants when they reach the desired maturity and optionally in separating the seeds from the harvested plants.

34. Method according to claim 33, characterized in that the particular herbicide is applied before sowing, before emergence or after emergence of the crop.